THE PERSONAL GENOME

Everyone has one ADELAIDE RHODES, PH.D.

IMPORTANCE OF PERSONAL GENOMES

PERSONAL GENOMICS FOR HEALTHCARE WILL EXCEED CLOUD DEMAND FOR CLINICAL AND ACADEMIC GENOMICS RESEARCH

THE U.S. SPENDS

BY 2024 \$340 BILLION

COMPUTING

DOLLARS/YEAR OF OVERALL WORLD FUNDING WILL BE SPENT ON ON GENOMICS CLOUD

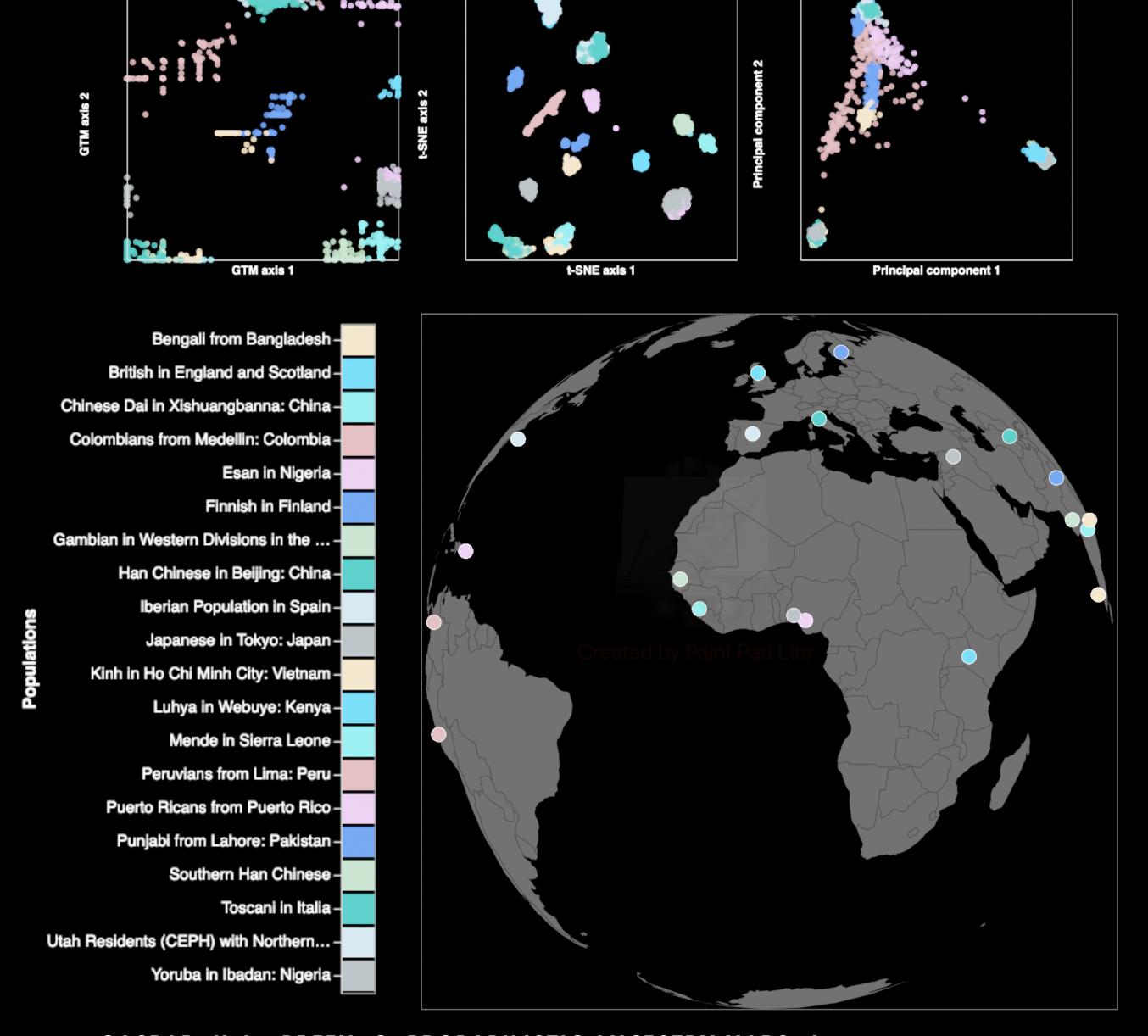
60 MILLION

WILL HAVE THEIR GENOME SEQUENCED IN A HEALTHCARE RESEARCH CONTEXT

BY 2025

Sources: https://www.marketwatch.com/press-release/global-cloud-computing-market-size-2019-industry-trends-share-statistics-worldwide-overview-key-players-analysis-research-by-types-services-regional-outlook-and-forecasts-till-2024-2019-11-13 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2576262/, https://www.cell.com/ajhg/fulltext/S0002-9297(18)30422-1

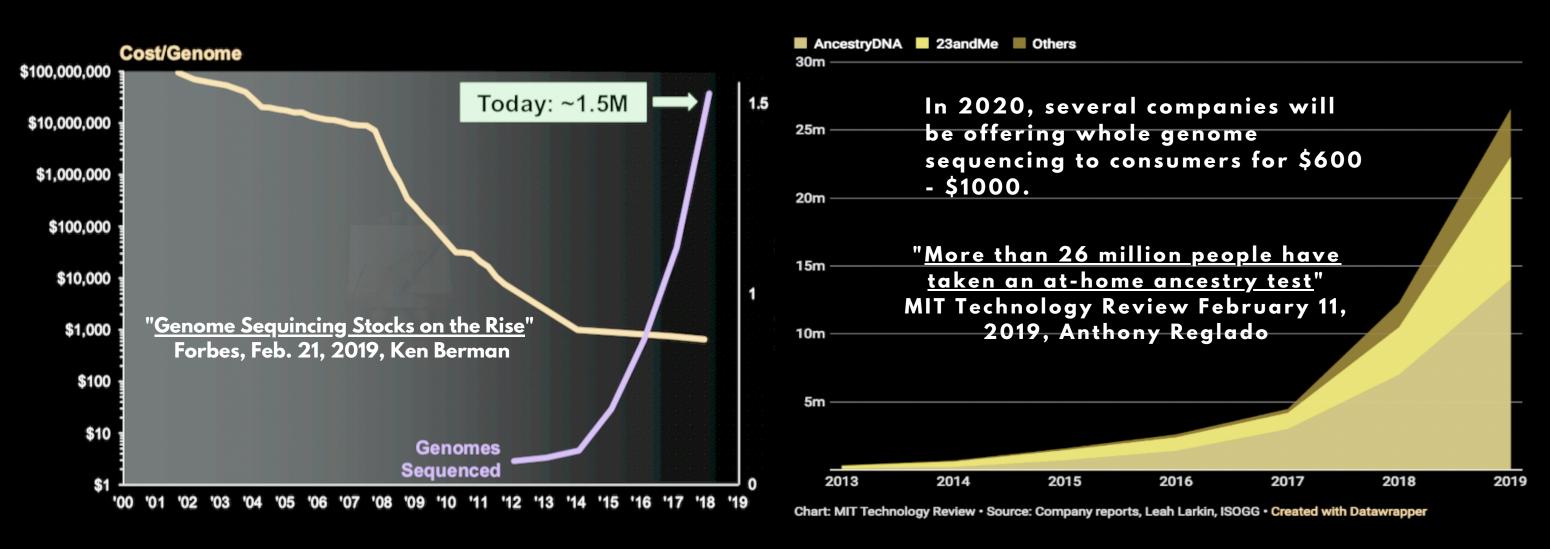
RESEARCHERS RELY ON INSIGHTS FROM PANGENOMES AND PERSONAL GENOMES



GASPAR, H.A., BREEN, G. PROBABILISTIC ANCESTRY MAPS: A METHOD TO ASSESS AND VISUALIZE POPULATION SUBSTRUCTURES IN GENETICS. BMC BIOINFORMATICS 20, 116 (2019). HTTPS://DOI.ORG/10.1186/S12859-019-2680-1

BIOINFORMATIC CONSIDERATIONS

MASSIVE AMOUNTS OF DATA



- EACH GENOME GENERATES 100 GB DATA FOR DOWNSTREAM ANALYSIS, • THIS REQUIRES STORAGE BEYOND WHAT THE TYPICAL HPC ACCOMMODATES
- 100 MILLION GENOMES X 100 GIGABYTES OF DATA = 10 EXABYTES OF DATA

NEED FOR INNOVATIVE TECHNOLOGY & **CLOUD-NATIVE ANALYSIS**

- NGS TOOLS ARE NOT CROSS-PLATFORM TOOLS. THE MAJORITY OF THEM WORK ON THE LINUX/UNIX OPERATING SYSTEM.
- MOST OF THE NGS TOOLS INTERACT WITH USERS VIA COMMAND LINE INTERFACE.
- VERY FEW NGS TOOLS HAVE BEEN DEVELOPED DURING THE LAST 5 YEARS.
- THERE IS NO STANDARD INPUT/OUTPUT FILE FORMAT FOR NGS TOOLS.

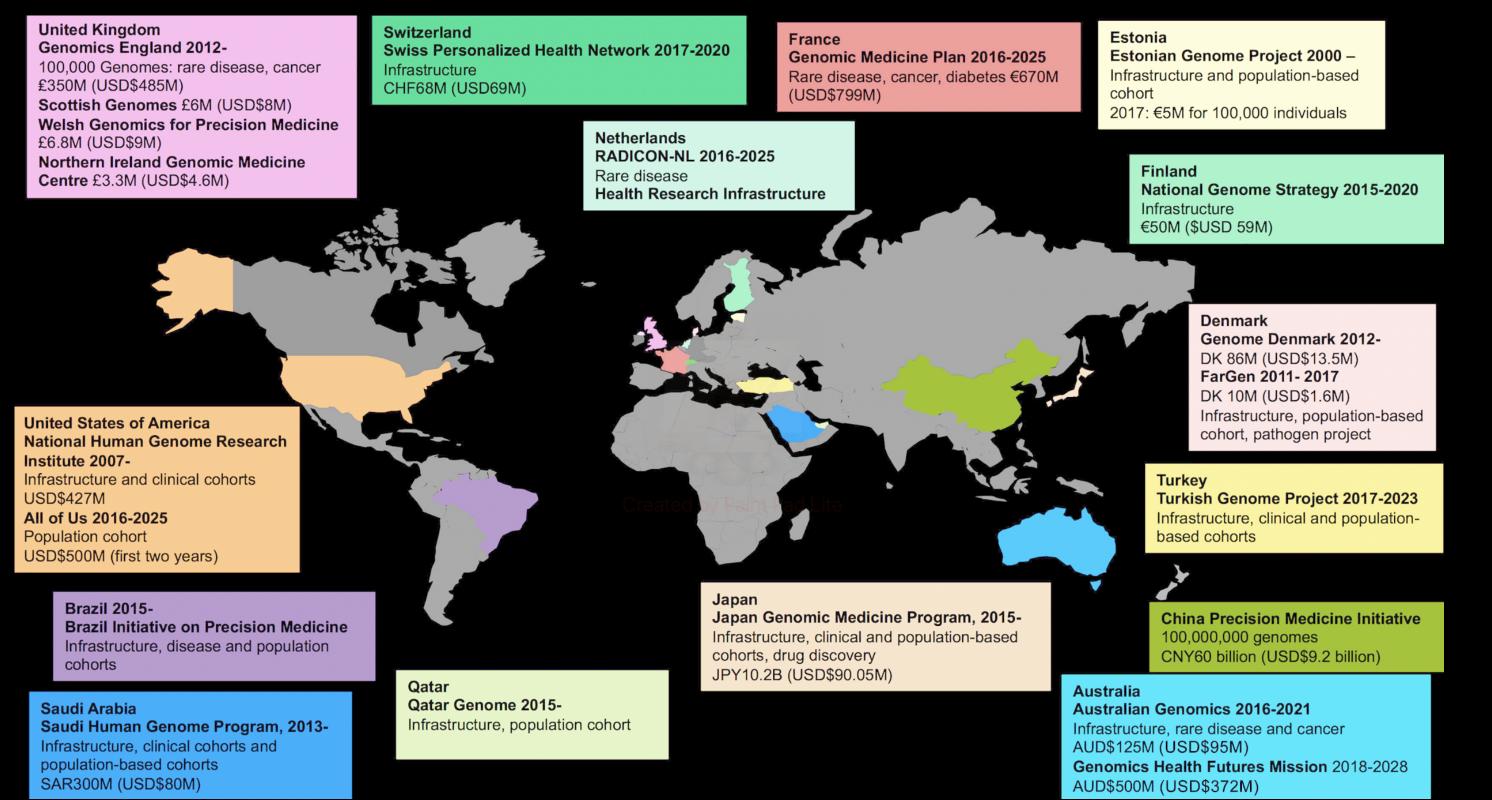
RESULT: REDUCED COMPATIBILITY, PORTABILITY, INTEROPERABILITY, AND INTEGRATION BETWEEN THE TOOLS.

FINDINGS FROM BANI BAKER ET AL. 2020 (DOI.ORG/10.1016/J.IMU.2020.100296)

SECURITY IN DATA COLLABORATIONS

"RESEARCHERS MUST BE ABLE TO RESPONSIBLY INTERROGATE THE WORLD'S COLLECTIVE GENOMIC DATA AS A SINGLE VIRTUAL COHORT THAT TRANSCENDS THE CAPACITY — AND JURISDICTION — OF ANY SINGLE ORGANISATION OR COUNTRY."

FROM ARTICLE - "ELIXIR AND GA4GH EXPAND COLLABORATION", MAY 2019 HTTPS://WWW.GA4GH.ORG/NEWS/ELIXIR-AND-GA4GH-EXPAND-COLLABORATION



STARK ET AL. INTEGRATING GENOMICS INTO HEALTHCARE: A GLOBAL RESPONSIBILITY. THE AMERICAN JOURNAL OF HUMAN GENETICS 104.1 (2019): 13-20.

NEED FOR CLOUD SOLUTIONS

PERSONAL GENOMES CAN BE COMPRESSED AND CONVERTED TO SEARCHABLE FORMATS

CLOUD SIMPLIFIES MAKING DATA F.A.I.R. = FINDABLE, ACCESSIBLE, INTEROPERABLE AND REUSABLE

- CONVERT GENOMIC VCF INTO COMPRESSED BIGQUERY OR ATHENA **FORMATS**
- USE REST API AND SQL TO SEARCH VARIANTS ACROSS GENOMES WITH SIMPLE COORDINATES OR PATTERN MATCHING
- MULTIPLE VARIANT SETS FOR PANGENOMES CAN BE JOINED WITH SIMPLE SQL COMMANDS
- PERSONAL GENOME DATA CAN BE LINK TO PUBLIC TEST DATA SETS SUCH AS 1000 GENOMES, SIMON GENOMES, PLATINUM GENOMES.
- RAW SEQUENCING DATA CAN BE MOVED TO ARCHIVAL STORAGE ONCE ALIGNMENTS ARE PRODUCED.

PERSONAL GENOMES BENEFIT FROM SCALABLE OPTIONS FOR MACHINE LEARNING TO OPTIMIZE COSTS AND REDUCE TIME

KUBEFLOW

- UTLIZES GPU'S (GRAPHICAL PROCESSING UNITS) TO SPEED UP **PROCESSING**
- PARTITION MULTIPLE JOBS ON ONE GPU
- CAN BE CONTROLLED FROM LOCAL MACHINE OR FROM A VM IN GCP

TENSORFLOW

- ALLOWS EXPANSION OF ML TO TPU'S (TENSOR PROCESSING UNITS)
- HIGHER MEMORY OPTIONS NOW AVAILABLE
- TAKES MINUTES TO COMPLETE VERSUS DAYS OR WEEKS.

PERSONAL GENOMES IN THE CLOUD CAN HAVE AUTOMATED ENCRYPTION AND SECURITY POLICIES

- DEVELOP AND AUTOMATE COMPLIANCE & CYBER RISK MANAGEMENT **PROCESSES**
- COMPLY WITH FISM, NIST RMF AND HIPAA
- SECURE GENOMICS DATA, PHI AND CLINICAL\TRANSLATIONAL RESEARCH DATA IN CLOUD ENVIRONMENTS
- AUTOMATE GA4GH, SSO AND CLOUD USAGE POLICIES



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ONIX ENABLES HEALTH AND LIFE SCIENCE ORGANIZATIONS TO REALIZE THE POWER OF THE CLOUD TO SECURELY WORK SIMPLER, SMARTER AND FASTER IN A HIPAA-COMPLIANT ENVIRONMENT.